REMARKS

Claim 176 was objected to, because the first line omitted the term "of" after "method". This informality has been addressed as reflected above in the "Listing of the Claims". Withdrawal of this objection is respectfully requested in view of this.

Claims 174 and 176 were rejected under 35 USC §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention.

Usage of the term "or" has been reduced in Claims 174 and 176.

The term "consisting essentially of" has been replaced by the term "comprising".

The "or part of" remains in the claims. The claims recite that all or part of a sequence is useful in cosuppressing an endogenous gene. The skilled in the art know that an entire coding region is not needed to down-regulate expression of a gene. Submitted herewith is a copy U.S. Patent No. 5,231,020 issued to Jorgensen et al. on July 27, 1993) (copy enclosed) supporting this very aspect. Attention is kindly invited to column 8 at lines 1-19 which states, *inter alia*, that ". . . It should be noted that since a full length coding sequence is unnecessary, it is possible to produce the same effect on multiple proteins together to coordinately repress various different genes." It is stated in column 8 at lines 9-14 that a "sequence of greater than 50-100 nucleotides should be used, though a sequence of greater than about 200-300 nucleotides would be preferred, and a sequence of greater than 500-1000 nucleotides would be especially preferred depending on the size of the endogenous gene. " All of this is information available to those of ordinary skill in the art.

In view of the foregoing discussion, it is respectfully submitted that use of the expression "or part of" is not indefinite since it is coupled with "useful in cosuppressing an endogenous gene. . . ."

A basis for comparison has been provided for the recitation "altered" in the expression "altered corn oil". Support for the foregoing can be found on page 17at lines 4-22 of the specification. Thus, it is believed that no new matter has been added.

Withdrawal of these grounds of rejection are respectfully requested in view of the amendments to the claims.

Claims 174 and 176 were rejected under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement for the reasons set forth in previous office actions.

It is respectfully submitted that the claims show a clear correlation between structure and function. The claims recite that all or part of an isolated nucleic acid sequence encoding a desaturase and that all or part of this sequence is useful in cosuppressing expression of an endogenous gene. Thus, it is respectfully submitted that the written description requirement has been fully satisfied for all of the reasons set forth herein and in the previously filed responses.

Claims 174 and 176 were rejected under 35 35 U.S.C. §112, first paragraph, as failing to comply with the enablement requirement. Concern was raised about the plasmid sequence of pBN431.

pBN431 is a derivative of plasmid vectors pBN427 (Fig. 7A) and pBN414 (Fig. 3E) and was assembled from one of the purified HIND III digest products obtained from each of these two plasmids. Specifically, a) part of the shrunken-1 intron, FAD2, the delta-9 desaturase, and the NOS 3' terminator from pBN 414 and b) the vector backbone with selection for Hygromycin, part of the shrunken-1 intron, the oleosin promoter and the T7 terminator from pBN427 were used to construct pBN431.

pBN414 and pB427 are described, in detail, in the specification on page 42, lines 21-26 (pBN414) and page 46, line 14 through page 47 line 3 (pBN427). Due to a clerical error, the drawing of Fig. 7C, depicting pBN431, incorrectly describes the location of the shrunken-1 and delta-12 desaturase and the identifier for the delta 12-Desaturase (FAD2) fragment was inadvertently omitted.

Support for this can be found in the instant application on page 50 at lines 17-21 which states that "[a]n alternative approach for obtaining a corn plant high in both saturated fatty acids and oleic acid is to create a transgenic line with a transgene construct containing the **fused fad2 and delta-9 desaturase genes, such as in pBN412 or pBN414 or pBN431**. . . ." (Emphasis added.) Thus, pBN431 should contain a fused fad2 and delta-9 desaturase genes.

Figure 7C of PCT publication (WO 99/64579, published December 16, 1999) of the above-identified application correctly depicts pBN431. WO 99/64579 and the

instant application both claim the benefit of priority of the same provisional application having Application No. 60/088987

A corrected drawing of pBN431(corresponding to Figure 7C of WO 99/64579) is submitted herewith and Applicants respectfully request replacement of current Fig. 7C with the attached correct drawing since it is believed that no new matter has been added.

Withdrawal of the rejection of the claims under 35 35 U.S.C. §112, first paragraph, as failing to comply with the enablement requirement is respectfully requested in view of the foregoing discussion.

Claims 174 and 176 were rejected under 35 U.S.C. §112, first paragraph as failing to comply with the enablement requirement.

Attention is kindly invited to the specification at page 6, lines 1 to 29, which discloses alterations in nucleotide sequence that are not expected to alter functionality, such as alterations that produce a chemically equivalent amino acid at a given site or alterations in the N- or C-terminal portions. Thus, from the foregoing, the skilled artisan would immediately understand the specification to disclose a representative number of polynucleotide sequences, having different nucleotide substitutions, that encode delta-9 stearoyl ACP desaturase or delta-12 desaturase but that vary from SEQ ID NO:1 and 9.

Attention is also invited to Shanklin et al. ((1991), PNAS 88: 2510-2514, copy enclosed.) Shanklin et al. discloses delta-9 desaturases isolated from *Ricinus communis* (gi:134945) and *Cucumis sativus* (gi: 417820).

Stearoyl-ACP or delta-9 desaturase activity of the sequence from *Ricinus communis* was confirmed by transforming yeast, an organism that does not posess a soluble stearoyl desaturase , with the sequence from *Ricinus communis*. Soluble ferredoxin-dependent delta-9 desaturase activity indistinguishable from that found in crude extracts of plant tissues was observed.

A comparison of the two protein sequences disclosed by Shanklin et al. and SEQ ID NO:9 is shown in Appendix A. The proteins from *Ricinus communis* (gi:134945) and *Cucumis sativus* (gi: 417820) share a sequence identity of 75.3% and 72.5%, respectively with SEQ ID NO:9. One skilled in the art would appreciate that the more highly conserved a residue is, the less likely that it could be modified and function maintained. Also, one skilled in the art could quickly determine which

amino acid residues might be modified in SEQ ID NO:9 without a likely change in function by reviewing the alignment set forth in the attached Appendix.

With respect to SEQ ID NO:1 and delta-12 desaturase, attention is kindly invited to WO 94/11516, published May 26, 1994, which describes genes for microsomal delta-12 desaturases, including a corn delta-12 desaturase and related enzymes from plants. Table 4 on page 44 of the before mentioned reference shows a comparison of the percent identity between the coding regions of nucleotide sequences encoding different microsomal delta-12 desaturases. The degree of overall identity between the plant delta-12 desaturase is above 60% at the nucleotide level, whereas the overall degree of identity at the amino acid level is 60% or greater (Table 5 , page 45 in WO 94/11516). Analysis of soybean embryos transformed with the soy delta-12 desaturase and canola seeds transformed with the canola delta-12 desaturase , confirmed the expected change in fatty acid profile (Table 12 & 13, page 95 and Table 14 & 15, pages 108-109 in WO 94/11516, respectively). Therefore, it would be expected that many variants sharing at least 90% sequence identity at the nucleotide level with SEQ ID NO:1 would have been expected to retain the claimed function.

Thus, given the correlation of structure and function as discussed above, it is respectfully submitted that one skilled in the art could make and use the claimed invention without engaging in undue experimentation.

A Petition for an Extension of Time of one (1) month accompanies this response along with copies of the reference discussed herein and cited on PTO/SB/08A and PTO/SB/08B forms.

In view of the foregoing, it is respectfully submitted that the claims are now in form for allowance which allowance is respectfully solicited.

Please charge any requisite fees associated with the filing of this response including, but not limited to, the Petition for Extension of time for one (1) month or credit any overpayment to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Respectfully submitted,

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APPENDIX A

Appendix A shows a comparison of the amino acid sequences of the corn delta-9 desaturase (SEQ ID NO:9) and the delta-9 desaturases from *Cucumis sativum* (gi: 417820) and *Ricinus communis* (gi: 134945). Identical amino acids are indicated with an asterix above the alignment. Dashes are used by the program to maximize alignment of the sequences.

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                ***                     *  *  *     *        *   *  **  **** ***
SEQ ID NO:9 MALRLHDV--------ALCLSPPLAARRRSGGSFVAVASMTSAAVSTRVEN-KKPFAPPR
GI: 417820  MALKFHPLTSQSPKLPSFRM-PQLASLRSP--KFVMASTLRST--SREVETLKKPFMPPR
GI: 134945  MALKLNPFLSQTQKLPSFAL-PPMASTRSP--KFYMASTLKSG--SKEVENLKKPFMPPR

                *** *******    ******  **  * * ****** ********** *  **   * *
SEQ ID NO:9 EVHVQVTHSMPSHKIEIFKSLDDWARDNILTHLKPVEKCWQPQDFLPDPASEGFHDEVKE
GI: 417820  EVHLQVTHSMPPQKMEIFKSLEDWAEENLLVHLKPVERCWQPQDFLPDSAFEGFHEQVRE
GI: 134945  EVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRE

                ******* ** *** ********************************** ** ********
SEQ ID NO:9 LRERAKEIPDDYFVCLVGDMITEEALPTYQTMLNTLDGVRDETGASPTAWAVWTRAWTAE
GI: 417820  LRERAKELPDEYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTPWAIWTRAWTAE
GI: 134945  LRERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAE

                *********** ** **** ** **********                  ******** **
SEQ ID NO:9 ENRHGDLLNKYMYLTGRVDIRQIEKTIQYLIGSVDIRQIEKTIQYLIGSGMDPRTENNPY
GI: 417820  ENRHGDLLNKYLYLSGRVDMRQVEKTIQYLIGS----------------GMDPRTENNPY
GI: 134945  ENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGS----------------GMDPRTENSPY

                *** ****************** *   ** ******* *  ********************
SEQ ID NO:9 LGFVYTSFQERATFISHGNTARHAKDFGDLKLAQICGIIASDEKRHETAYTKIVEKLFEI
GI: 417820  LGFIYTSFQERATFISHGNTARLAKEHGDIKLAQICGTITADEKRHETAYTKIVEKLFEI
GI: 134945  LGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEI

                ** *** *   ** ** ******* ** ** ** *** ********** **********
SEQ ID NO:9 DPDGTVVALADMMKKKISMPAHLMFDGQDDKLFEHFSMVAQRLGVYTARDYADILEFLVD
GI: 417820  DPEGTVIAFEEMMRKKVSMPAHLMYDGRDDNLFHHFSAVAQRLGVYTAKDYADILEFLVG
GI: 134945  DPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADILEFLVG

                ****  ***** ** ****  * *  *** * **** ***   * ****   * *
SEQ ID NO:9 RWKVADLTGLSGEGNKAQDYLCTLASRIRRLDERAQSRAKKAGTLPFSWVYGREVQL.
GI: 417820  RWKVESLTGLSGEGQKAQDYVCALPARIRKLEERAQGRAKEGPTIPFSWIFDRQVK-L
GI: 134945  RWKVDKLTGLSAEGQKAQDYVCRLPPRIRRLEERAQGRAKEAPTMPFSWIFDRQVK-L
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